

R045FR11 APP
LISTE DE SEQUENCES

<110> CYTOMICS SYSTEMS

<120> Procédé de criblage in vitro d'agents modulant
l'ubiquitination de la protéine I-Kappa-B-Alpha et
moyens destinés à la mise en oeuvre dudit procédé

<130> CYTOMICS

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<170> PatentIn Ver. 2.1

<210> 1

<211> 1719

<212> ADN

<213> Séquence artificielle

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<223> Description de la séquence
artificielle:GFP-NLS-IkBa

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artificielle:GFP-NLS-IkBa

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Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
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Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
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Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
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Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
195 200 205

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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln
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Asp Gly Leu Lys Lys Glu Arg Leu Leu Asp Asp Arg His Asp Ser Gly
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Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu Leu
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Gln Glu Ile Arg Leu Glu Pro Gln Glu Val Pro Arg Gly Ser Glu Pro

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Lys Gly Asp₃₅₅ Leu Ala Phe Leu Asn₃₆₀ Phe Gln Asn Asn Leu₃₆₅ Gln Gln Thr
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Leu₃₈₅ Leu Gly Ala Gly Cys₃₉₀ Asp Pro Glu Leu Arg₃₉₅ Asp Phe Arg Gly Asn₄₀₀
Thr Pro Leu His Leu₄₀₅ Ala Cys Glu Gln Gly₄₁₀ Cys Leu Ala Ser Val₄₁₅ Gly
Val Leu Thr Gln₄₂₀ Ser Cys Thr Thr Pro₄₂₅ His Leu His Ser Ile₄₃₀ Leu Lys
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Trp Gly Arg₅₁₅ Pro Ser Thr Arg Ile₅₂₀ Gln Gln Gln Leu Gly₅₂₅ Gln Leu Thr
Leu Glu Asn Leu Gln Met Leu₅₃₅ Pro Glu Ser Glu Asp₅₄₀ Glu Glu Ser Tyr
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 35 40 45

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Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
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 Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
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 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
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 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
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 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
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 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
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 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
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 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
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 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
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 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Leu Gln
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 245 250 255
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 305 310 315 320
 Pro Arg Lys Ile Ile Pro Glu Lys Asn Ser Leu Arg Gln Thr Tyr Asn
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 Ser Cys Ala Arg Leu Cys Leu Asn Gln Glu Thr Val Cys Leu Ala Ser
 340 345 350
 Thr Ala Met Lys Thr Glu Asn Cys Val Ala Lys Thr Lys Leu Ala Asn
 355 360 365
 Gly Thr Ser Ser Met Ile Val Pro Lys Gln Arg Lys Leu Ser Ala Ser
 370 375 380

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Tyr Glu Lys Glu Lys Glu Leu Cys Val Lys Tyr Phe Glu Gln Trp Ser
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 His Tyr Gln His Gly His Ile Asn Ser Tyr Leu Lys Pro Met Leu Gln
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 465 470 475 480
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Phe Asp Asn Lys Arg Ile Val Ser Gly Ala Tyr Asp Gly Lys Ile Lys
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Val Trp Asp Leu Val Ala Ala Leu Asp Pro Arg Ala Pro Ala Gly Thr
785 790 795 800
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Gln Phe Asp Glu Phe Gln Ile Val Ser Ser Ser His Asp Asp Thr Ile
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